



09729141.1029037

# SEQUENCE LISTING

<110> Logemann, Juergen  
Jach, Guido  
Gornhardt, Birgit  
Mundy, John  
Schell, Jeff  
Eckes, Peter  
Chet, Ilan

<120> Transgenic pathogen-resistant organism

<130> A29542-FWC-I-R 070037.0195

<140> US 09/729,141

<141> 2000-12-01

<150> 08/812,025

<151> 1997-03-06

<150> 08/457,797

<151> 1995-06-01

<150> 08/134,416

<151> 1993-10-08

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Arg Ala Arg Val Leu Ala Thr Tyr Asn Gly Lys Cys Tyr Lys Lys Asp  
5 10 15 20

aat atc tgc aag tac aag gca cag agc ggc aag act gcc att tgc aag 153  
 Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr Ala Ile Cys Lys  
                   25                                  30                                  35

tgc tat gtc aaa aag tgc ccc cgc gac ggc gcg aaa tgc gag ttt gac 201  
 Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys Cys Glu Phe Asp  
                   40                                  45                                  50

agc tac aag ggg aag tgc tac tgc tagacggtga gcgaagggac gaagtaggct 255  
 Ser Tyr Lys Gly Lys Cys Tyr Cys  
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ggggggttatt ttactctgct 275

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 <213> Aspergillus giganteus

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 Tyr Lys Lys Asp Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr  
                   20                  25                  30  
 Ala Ile Cys Lys Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys  
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 Cys Glu Phe Asp Ser Tyr Lys Gly Lys Cys Tyr Cys  
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<210> 3  
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 <213> Aspergillus giganteus

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 Lys Ala Gln Ser Gly Lys Thr Ala Ile Cys Lys Cys Tyr Val Lys Lys  
                   20                  25                  30  
 Cys Pro Arg Asp Gly Ala Lys Cys Glu Phe Asp Ser Tyr Lys Gly Lys  
                   35                  40                  45  
 Cys Tyr Cys  
           50

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 <213> Hordeum vulgare

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<222> (886)...(1032)

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<221> polyA\_signal

<222> (930)...(935)

<223> potential polyadenylation signal

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atg gcg aag aac gtg gac aag ccg ctc ttc acc gcg acg ttc aac gtc	102
Met Ala Lys Asn Val Asp Lys Pro Leu Phe Thr Ala Thr Phe Asn Val	
5 10 15 20	

cag gcc agc tcc gcc gac tac gcc acc ttc atc gcc ggc atc cgc aac	150
Gln Ala Ser Ser Ala Asp Tyr Ala Thr Phe Ile Ala Gly Ile Arg Asn	
25 30 35	

aag ctc cgc aac ccg gcg cac ttc tcc cac aac cgc ccc gtg ctg ccg	198
Lys Leu Arg Asn Pro Ala His Phe Ser His Asn Arg Pro Val Leu Pro	
40 45 50	

ccg gtc gag ccc aac gtc ccg ccg agc agg tgg ttc cac gtc gtg ctc	246
Pro Val Glu Pro Asn Val Pro Pro Ser Arg Trp Phe His Val Val Leu	
55 60 65	

aag gcc tcg ccg acc agc gcc ggg ctc acg ctg gcc att cgg gcg gac	294
Lys Ala Ser Pro Thr Ser Ala Gly Leu Thr Leu Ala Ile Arg Ala Asp	

70	75	80	
aac atc tac ctg gag ggc ttc aag agc agc gac ggc acc tgg tgg gag Asn Ile Tyr Leu Glu Gly Phe Lys Ser Ser Asp Gly Thr Trp Trp Glu 85 90 95 100			342
ctc acc ccg ggc ctc atc ccc ggc gcc acc tac gtc ggg ttc ggc ggc Leu Thr Pro Gly Leu Ile Pro Gly Ala Thr Tyr Val Gly Phe Gly Gly 105 110 115			390
acc tac cgc gac ctc ctc ggc gac acc gac aag ctg acc aac gtc gct Thr Tyr Arg Asp Leu Leu Gly Asp Thr Asp Lys Leu Thr Asn Val Ala 120 125 130			438
ctc ggc cgg cag cag ctg gcg gac gcg gtg acc gcc ctc cac ggg cgc Leu Gly Arg Gln Gln Leu Ala Asp Ala Val Thr Ala Leu His Gly Arg 135 140 145			486
acc aag gcc gac aag ccg tcc ggc ccg aag cag cag cag gcg agg gag Thr Lys Ala Asp Lys Pro Ser Gly Pro Lys Gln Gln Gln Ala Arg Glu 150 155 160			534
gcg gtg acg acg ctg ctc ctc atg gtg aac gag gcc acg ccg ttc cag Ala Val Thr Thr Leu Leu Leu Met Val Asn Glu Ala Thr Arg Phe Gln 165 170 175 180			582
acg gtg tct ggg ttc gtg gcc ggc ttg ctg cac ccc aag gcg gtg gag Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro Lys Ala Val Glu 185 190 195			630
aag aag agc ggg aag atc ggc aat gag atg aag gcc cag gtg aac ggg Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala Gln Val Asn Gly 200 205 210			678
tgg cag gac ctg tcc gcg gcg ctg ctg aag acg gac gtg aag cct ccg Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro 215 220 225			726
ccg gga aag tcg cca gcg aag ttc gcg ccg atc gag aag atg ggc gtg Pro Gly Lys Ser Pro Ala Lys Phe Ala Pro Ile Glu Lys Met Gly Val 230 235 240			774
agg acg gct gta cag gcc gcc aac acg ctg ggg atc ctg ctg ttc gtg Arg Thr Ala Val Gln Ala Ala Asn Thr Leu Gly Ile Leu Leu Phe Val 245 250 255 260			822
gag gtg ccg ggt ggg ttg acg gtg gcc aag gcg ctg gag ctg ttc cat Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu Glu Leu Phe His 265 270 275			870

gcg agt ggt ggg aaa taggtagttt tccaggtata cctgcatggg tagtgtaaaa 925  
 Ala Ser Gly Gly Lys  
 280

gtcgaataaa catgtcacag agtgacggac tgatataaat aaataaataa acgtgtcaca 985  
 gagttacata taaacaaata aataaataat taaaaatgtc cagttta 1032

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 <211> 281  
 <212> PRT  
 <213> Hordeum vulgare

<400> 5  
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 Gly Ile Arg Asn Lys Leu Arg Asn Pro Ala His Phe Ser His Asn Arg  
 35 40 45  
 Pro Val Leu Pro Pro Val Glu Pro Asn Val Pro Pro Ser Arg Trp Phe  
 50 55 60  
 His Val Val Leu Lys Ala Ser Pro Thr Ser Ala Gly Leu Thr Leu Ala  
 65 70 75 80  
 Ile Arg Ala Asp Asn Ile Tyr Leu Glu Gly Phe Lys Ser Ser Asp Gly  
 85 90 95  
 Thr Trp Trp Glu Leu Thr Pro Gly Leu Ile Pro Gly Ala Thr Tyr Val  
 100 105 110  
 Gly Phe Gly Gly Thr Tyr Arg Asp Leu Leu Gly Asp Thr Asp Lys Leu  
 115 120 125  
 Thr Asn Val Ala Leu Gly Arg Gln Gln Leu Ala Asp Ala Val Thr Ala  
 130 135 140  
 Leu His Gly Arg Thr Lys Ala Asp Lys Pro Ser Gly Pro Lys Gln Gln  
 145 150 155 160  
 Gln Ala Arg Glu Ala Val Thr Thr Leu Leu Leu Met Val Asn Glu Ala  
 165 170 175  
 Thr Arg Phe Gln Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro  
 180 185 190  
 Lys Ala Val Glu Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala  
 195 200 205  
 Gln Val Asn Gly Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp  
 210 215 220  
 Val Lys Pro Pro Pro Gly Lys Ser Pro Ala Lys Phe Ala Pro Ile Glu  
 225 230 235 240  
 Lys Met Gly Val Arg Thr Ala Val Gln Ala Ala Asn Thr Leu Gly Ile  
 245 250 255  
 Leu Leu Phe Val Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu  
 260 265 270  
 Glu Leu Phe His Ala Ser Gly Gly Lys  
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<210> 6  
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 <212> DNA  
 <213> Hordeum vulgare

<220>  
 <221> CDS  
 <222> (1)...(351)  
 <223> protein synthesis inhibitor (PSI), aminoterminally  
 incomplete protein from an incomplete PSI cDNA  
 clone

<221> 3'UTR  
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 <222> (404)...(409)  
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1				5					10					15		
acg	gtg	tcg	ggg	ttc	gtg	gcc	ggg	ctg	ctg	cac	ccc	aag	gcg	gtg	gag	96
Thr	Val	Ser	Gly	Phe	Val	Ala	Gly	Leu	Leu	His	Pro	Lys	Ala	Val	Glu	
			20					25					30			
aag	aag	agc	ggg	aag	atc	ggc	aat	gag	atg	aag	gcc	cag	gtg	aac	ggg	144
Lys	Lys	Ser	Gly	Lys	Ile	Gly	Asn	Glu	Met	Lys	Ala	Gln	Val	Asn	Gly	
		35				40						45				
tgg	cag	gac	ctg	tcc	gcg	gcg	ctg	ctg	aag	acg	gac	gtg	aag	ccc	ccg	192
Trp	Gln	Asp	Leu	Ser	Ala	Ala	Leu	Leu	Lys	Thr	Asp	Val	Lys	Pro	Pro	
	50					55					60					
ccg	gga	aag	tcg	cca	gcg	aag	ttc	acg	ccg	atc	gag	aag	atg	ggc	gtg	240
Pro	Gly	Lys	Ser	Pro	Ala	Lys	Phe	Thr	Pro	Ile	Glu	Lys	Met	Gly	Val	
65					70					75					80	
agg	act	gct	gag	cag	gct	gcg	gct	act	ttg	ggg	atc	ctg	ctg	ttc	gtt	288

Arg Thr Ala Glu Gln Ala Ala Ala Thr Leu Gly Ile Leu Leu Phe Val  
                     85                    90                    95

gag gtg ccg ggt ggg ttg acg gtg gcc aag gcg ctg gag ctg ttt cat 336  
 Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu Glu Leu Phe His  
                     100                    105                    110

gcg agt ggt ggg aaa taggtagttt tgcagggtata cctgcatggg taaatgtaaa 391  
 Ala Ser Gly Gly Lys  
                     115

agtcgaataa aaatgtcaca gagtgacgga ctgatataaa taaattaata aacatgtcat 451  
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 <211> 117  
 <212> PRT  
 <213> Hordeum vulgare

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                     20                    25                    30  
 Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala Gln Val Asn Gly  
                     35                    40                    45  
 Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro  
   50                    55                    60  
 Pro Gly Lys Ser Pro Ala Lys Phe Thr Pro Ile Glu Lys Met Gly Val  
  65                    70                    75                    80  
 Arg Thr Ala Glu Gln Ala Ala Ala Thr Leu Gly Ile Leu Leu Phe Val  
                     85                    90                    95  
 Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu Glu Leu Phe His  
                     100                    105                    110  
 Ala Ser Gly Gly Lys  
                     115

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 <213> Serratia marcescens

<220>  
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 <223> ChiS gene from plasmid pLChis from E.coli A5187

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<223> 26 kD preprotein of chitinase (ChiG)

<221> 3'UTR

<222> (862)...(1002)

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<222> (905)...(910)

<223> potential polyadenylation site

<221> sig\_peptide

<222> (64)...(294)

<223> probable signal peptide

<221> sig\_peptide

<222> (298)...(312)

<223> probable signal peptide

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<222> (349)...(378)

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<222> (466)...(588)

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<222> (607)...(861)

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<222> (133)...(861)

<400> 9

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aca atg aga tcg ctc gcg gtg gtg gtg gcc gtg gta gcc acg gtg gcc 108
    Met Arg Ser Leu Ala Val Val Val Ala Val Val Ala Thr Val Ala
      1              5              10              15

atg gcc atc ggc acg gcg cgc ggc agc gtg tcc tcc atc gtc tcg cgc 156
Met Ala Ile Gly Thr Ala Arg Gly Ser Val Ser Ser Ile Val Ser Arg
      20              25              30

gca cag ttt gac cgc atg ctt ctc cac cgc aac gac ggc gcc tgc cag 204
Ala Gln Phe Asp Arg Met Leu Leu His Arg Asn Asp Gly Ala Cys Gln
      35              40              45

gcc aag ggc ttc tac acc tac gac gcc ttc gtc gcc gcc gca gcc gcc 252
Ala Lys Gly Phe Tyr Thr Tyr Asp Ala Phe Val Ala Ala Ala Ala Ala
      50              55              60

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ttc Phe	ccg Pro 65	ggc Gly	ttc Phe	ggc Gly	acc Thr 70	acc Thr	ggc Gly	agc Ser	gcc Ala	gac Asp	gcc Ala 75	cag Gln	aag Lys	cgc Arg	gag Glu	300
gtg Val 80	gcc Ala	gcc Ala	ttc Phe	cta Leu	gca Ala 85	cag Gln	acc Thr	tcc Ser	cac His	gag Glu 90	acc Thr	acc Thr	ggc Gly	ggg Gly	tgg Trp 95	348
gcg Ala	act Thr	gca Ala	ccg Pro	gac Asp 100	ggg Gly	gcc Ala	ttc Phe	gcc Ala	tgg Trp 105	ggc Gly	tac Tyr	tgc Cys	ttc Phe	aag Lys 110	cag Gln	396
gaa Glu	cgt Arg	ggc Gly	gcc Ala 115	tcc Ser	tcc Ser	gac Asp	tac Tyr	tgc Cys 120	acc Thr	ccg Pro	agc Ser	gca Ala	caa Gln 125	tgg Trp	ccg Pro	444
tgc Cys	gcc Ala	ccc Pro 130	ggg Gly	aag Lys	cgc Arg	tac Tyr	tac Tyr 135	ggc Gly	cgc Arg	ggg Gly	cca Pro	atc Ile 140	cag Gln	ctc Leu	tcc Ser	492
cac His	aac Asn 145	tac Tyr	aac Asn	tat Tyr	gga Gly	cct Pro 150	gcc Ala	ggc Gly	cgg Arg	gcc Ala	atc Ile 155	ggg Gly	gtc Val	gat Asp	ctg Leu	540
ctg Leu 160	gcc Ala	aac Asn	ccg Pro	gac Asp	ctg Leu 165	gtg Val	gcc Ala	acg Thr	gac Asp	gcc Ala 170	act Thr	gtg Val	ggc Gly	ttt Phe	aag Lys 175	588
acg Thr	gcc Ala	atc Ile	tgg Trp	ttc Phe 180	tgg Trp	atg Met	acg Thr	gcg Ala	cag Gln 185	ccg Pro	ccc Pro	aag Lys	cca Pro	tcg Ser 190	agc Ser	636
cat His	gct Ala	gtg Val	atc Ile 195	gcc Ala	ggc Gly	cag Gln	tgg Trp	agc Ser 200	ccg Pro	tca Ser	ggg Gly	gct Ala	gac Asp 205	cgg Arg	gcc Ala	684
gca Ala	ggc Gly	cgg Arg 210	gtg Val	ccc Pro	ggg Gly	ttt Phe	ggt Gly 215	gtg Val	atc Ile	acc Thr	aac Asn	atc Ile 220	atc Ile	aac Asn	ggc Gly	732
ggg Gly	atc Ile 225	gag Glu	tgc Cys	ggt Gly	cac His	ggg Gly 230	cag Gln	gac Asp	agc Ser	cgc Arg	gtc Val 235	gcc Ala	gat Asp	cga Arg	atc Ile	780
ggg Gly	ttt Phe	tac Tyr	aag Lys	cgc Arg	tac Tyr	tgt Cys	gac Asp	atc Ile	ctc Leu	ggc Gly	gtt Val	ggc Gly	tac Tyr	ggc Gly	aac Asn	828

255

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aatcttggcc  ctccataaaa  tacaataaga  gcatcgtctc  ctatctacat  gctgtaagat  941
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<212> PRT
<213> Hordeum vulgare
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Gln	Phe	Asp 35	Arg	Met	Leu	Leu	His 40	Arg	Asn	Asp	Gly	Ala 45	Cys	Gln	Ala
Lys	Gly 50	Phe	Tyr	Thr	Tyr	Asp 55	Ala	Phe	Val	Ala	Ala 60	Ala	Ala	Ala	Phe
Pro 65	Gly	Phe	Gly	Thr	Thr 70	Gly	Ser	Ala	Asp	Ala 75	Gln	Lys	Arg	Glu 80	Val
Ala	Ala	Phe	Leu	Ala 85	Gln	Thr	Ser	His	Glu 90	Thr	Thr	Gly	Gly	Trp 95	Ala
Thr	Ala	Pro	Asp 100	Gly	Ala	Phe	Ala	Trp 105	Gly	Tyr	Cys	Phe	Lys 110	Gln	Glu
Arg	Gly	Ala 115	Ser	Ser	Asp	Tyr	Cys 120	Thr	Pro	Ser	Ala	Gln	Trp	Pro	Cys
Ala	Pro 130	Gly	Lys	Arg	Tyr	Tyr 135	Gly	Arg	Gly	Pro	Ile 140	Gln	Leu	Ser	His
Asn 145	Tyr	Asn	Tyr	Gly	Pro 150	Ala	Gly	Arg	Ala	Ile 155	Gly	Val	Asp	Leu	Leu 160
Ala	Asn	Pro	Asp	Leu 165	Val	Ala	Thr	Asp	Ala 170	Thr	Val	Gly	Phe	Lys 175	Thr
Ala	Ile	Trp	Phe 180	Trp	Met	Thr	Ala	Gln 185	Pro	Pro	Lys	Pro	Ser 190	Ser	His
Ala	Val	Ile 195	Ala	Gly	Gln	Trp	Ser 200	Pro	Ser	Gly	Ala	Asp 205	Arg	Ala	Ala
Gly	Arg 210	Val	Pro	Gly	Phe	Gly 215	Val	Ile	Thr	Asn	Ile 220	Ile	Asn	Gly	Gly
Ile 225	Glu	Cys	Gly	His	Gly 230	Gln	Asp	Ser	Arg	Val 235	Ala	Asp	Arg	Ile	Gly 240
Phe	Tyr	Lys	Arg	Tyr 245	Cys	Asp	Ile	Leu	Gly 250	Val	Gly	Tyr	Gly	Asn 255	Asn
Leu	Asp	Cys	Tyr 260	Ser	Gln	Arg	Pro	Phe 265	Ala						

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 <213> Hordeum vulgare

<220>  
 <221> 5'UTR  
 <222> (1)...(48)

<221> CDS  
 <222> (49)...(1050)  
 <223> preprotein of the glucanase GluG

<221> 3'UTR  
 <222> (1051)...(1235)  
 <223> partial, 14 nucleotides at the 3' end not shown

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 <222> (1083)...(1088)  
 <223> potential polyadenylation signal

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 <222> (1210)...(1215)  
 <223> potential polyadenylation signal

<221> mat\_peptide  
 <222> (133)...(1050)

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 Met Ala Arg  
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 Lys Asp Val Ala Ser Met Phe Ala Val Ala Leu Phe Ile Gly Ala Phe  
 5 10 15

gct gct gtt cct acg agt gtg cag tcc atc ggc gta tgc tac ggc gtg 153  
 Ala Ala Val Pro Thr Ser Val Gln Ser Ile Gly Val Cys Tyr Gly Val  
 20 25 30 35

atc ggc aac aac ctc ccc tcc cgg agc gac gtg gtg cag ctc tac agg 201  
 Ile Gly Asn Asn Leu Pro Ser Arg Ser Asp Val Val Gln Leu Tyr Arg  
 40 45 50

tcc aag ggc atc aac ggc atg cgc atc tac ttc gcc gac ggg cag gcc 249  
 Ser Lys Gly Ile Asn Gly Met Arg Ile Tyr Phe Ala Asp Gly Gln Ala  
 55 60 65

ctc	tcg	gcc	gtc	cgc	aac	tcc	ggc	atc	ggc	ctc	atc	ctc	gac	atc	ggc	297
Leu	Ser	Ala	Val	Arg	Asn	Ser	Gly	Ile	Gly	Leu	Ile	Leu	Asp	Ile	Gly	
		70					75					80				
aac	gac	cag	ctc	gcc	aac	atc	gcc	gcc	agc	acc	tcc	aac	gcg	gcc	tcc	345
Asn	Asp	Gln	Leu	Ala	Asn	Ile	Ala	Ala	Ser	Thr	Ser	Asn	Ala	Ala	Ser	
	85					90					95					
tgg	gtc	cag	aac	aac	gtg	cgg	ccc	tac	tac	cct	gcc	gtg	aac	atc	aag	393
Trp	Val	Gln	Asn	Asn	Val	Arg	Pro	Tyr	Tyr	Pro	Ala	Val	Asn	Ile	Lys	
100					105					110					115	
tac	atc	gcc	gcc	ggc	aac	gag	gtg	cag	ggc	ggc	gcc	acg	cag	agc	atc	441
Tyr	Ile	Ala	Ala	Gly	Asn	Glu	Val	Gln	Gly	Gly	Ala	Thr	Gln	Ser	Ile	
				120					125					130		
ctg	ccg	gcc	atg	cgc	aac	ctc	aac	gcg	gcc	ctc	tcc	gcg	gcg	ggg	ctc	489
Leu	Pro	Ala	Met	Arg	Asn	Leu	Asn	Ala	Ala	Leu	Ser	Ala	Ala	Gly	Leu	
			135					140						145		
ggc	gcc	atc	aag	gtg	tcc	acc	tcc	atc	cgg	ttc	gac	gag	gtg	gcc	aac	537
Gly	Ala	Ile	Lys	Val	Ser	Thr	Ser	Ile	Arg	Phe	Asp	Glu	Val	Ala	Asn	
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tcc	ttc	ccg	ccc	tcc	gcc	ggc	gtg	ttc	aag	aac	gcc	tac	atg	acg	gac	585
Ser	Phe	Pro	Pro	Ser	Ala	Gly	Val	Phe	Lys	Asn	Ala	Tyr	Met	Thr	Asp	
	165					170					175					
gtg	gcc	cgg	ctc	ctg	gcg	agc	acc	ggc	gcg	ccg	ctg	ctc	gcc	aac	gtc	633
Val	Ala	Arg	Leu	Leu	Ala	Ser	Thr	Gly	Ala	Pro	Leu	Leu	Ala	Asn	Val	
180					185					190					195	
tac	ccc	tac	ttc	gcg	tac	cgt	gac	aac	ccc	ggg	agc	atc	agc	ctg	aac	681
Tyr	Pro	Tyr	Phe	Ala	Tyr	Arg	Asp	Asn	Pro	Gly	Ser	Ile	Ser	Leu	Asn	
				200					205					210		
tac	gcg	acg	ttc	cag	ccg	ggc	acc	acc	gtg	cgt	gac	cag	aac	aac	ggg	729
Tyr	Ala	Thr	Phe	Gln	Pro	Gly	Thr	Thr	Val	Arg	Asp	Gln	Asn	Asn	Gly	
			215				220						225			
ctg	acc	tac	acg	tcc	ctg	ttc	gac	gcg	atg	gtg	gac	gcc	gtg	tac	gcg	777
Leu	Thr	Tyr	Thr	Ser	Leu	Phe	Asp	Ala	Met	Val	Asp	Ala	Val	Tyr	Ala	
		230					235					240				
gcg	ctg	gag	aag	gcc	ggc	gcg	ccg	gcg	gtg	aag	gtg	gtg	gtg	tcg	gag	825
Ala	Leu	Glu	Lys	Ala	Gly	Ala	Pro	Ala	Val	Lys	Val	Val	Val	Ser	Glu	
	245				250						255					
agc	ggg	tgg	ccg	tcg	gcg	ggc	ggg	ttt	gcg	gcg	tcg	gcc	ggc	aat	gcg	873



				165					170					175		
Met	Thr	Asp	Val	Ala	Arg	Leu	Leu	Ala	Ser	Thr	Gly	Ala	Pro	Leu	Leu	
			180					185					190			
Ala	Asn	Val	Tyr	Pro	Tyr	Phe	Ala	Tyr	Arg	Asp	Asn	Pro	Gly	Ser	Ile	
		195					200					205				
Ser	Leu	Asn	Tyr	Ala	Thr	Phe	Gln	Pro	Gly	Thr	Thr	Val	Arg	Asp	Gln	
	210					215					220					
Asn	Asn	Gly	Leu	Thr	Tyr	Thr	Ser	Leu	Phe	Asp	Ala	Met	Val	Asp	Ala	
225					230					235					240	
Val	Tyr	Ala	Ala	Leu	Glu	Lys	Ala	Gly	Ala	Pro	Ala	Val	Lys	Val	Val	
				245				250						255		
Val	Ser	Glu	Ser	Gly	Trp	Pro	Ser	Ala	Gly	Gly	Phe	Ala	Ala	Ser	Ala	
			260					265					270			
Gly	Asn	Ala	Arg	Thr	Tyr	Asn	Gln	Gly	Leu	Ile	Asn	His	Val	Gly	Gly	
		275					280					285				
Gly	Thr	Pro	Lys	Lys	Arg	Glu	Ala	Leu	Glu	Thr	Tyr	Ile	Phe	Ala	Met	
	290					295					300					
Phe	Asn	Glu	Asn	Gln	Lys	Thr	Gly	Asp	Ala	Thr	Glu	Arg	Ser	Phe	Gly	
305					310					315					320	
Leu	Phe	Asn	Pro	Asp	Lys	Ser	Pro	Ala	Tyr	Asn	Ile	Gln	Phe			
				325					330							